

In the Specification:

On page 27, please delete the paragraph beginning at line 17, and replace with:

Design of selector peptides: Synthetic peptides are used as catcher agents when isolating suitable single chain Fv (scFv) molecules from a phage-display library. The peptides are designed to capture phage particles displaying scFv with affinity to a C-terminal tetrapeptide in which the last (i.e. C-terminal) amino acid was either a lysine or and arginine. A spacer can be added on the N-terminal side of this tetrapeptide as well as an N-terminal biotin. The amino acid sequences are designed to include amino acids that are likely to generate good epitopes, such as hydrophobic amino acids (phenylalanine, tyrosine, tryptophan, leucine and isoleucine) or charged amino acids (aspartate, glutamate, asparagine, glutamine and histidine). Methionine is excluded due to its tendency to oxidise, and cysteine is excluded to avoid problems with dimerisation due to disulphide bridge formation. The sequences of the tetrapeptides are also decided based on their frequency in naturally occurring protein. Examples of suitable sequences are biotin-SGSG-XXX-COOH (SEQ ID NO. 1) where XXXX can be e.g., EDFR (SEQ ID NO. 2), EPER (SEQ ID NO. 3), HPDK (SEQ ID NO. 5), LPSR (SEQ ID NO. 6), LQSK (SEQ ID NO. 7), PEEK (SEQ ID NO. 8), WDSR (SEQ ID NO. 10) or YLDK (SEQ ID NO. 11).

On page 35, line 2, please replace table 2 with:

Name	Sequence
FN1	Biotin-SGSG-EDFR (-COOH) (<u>SEQ ID NO. 2</u>)
FN2	Biotin-SGSG-EPER (-COOH) (<u>SEQ ID NO. 3</u>)
FN3	Biotin-SGSG-EPFR (-COOH) (<u>SEQ ID NO. 4</u>)

Name	Sequence
FN4	Biotin-SGSG-HPDK(-COOH) <u>(SEQ ID NO. 5)</u>
FN5	Biotin-SGSG-LPSR(-COOH) <u>(SEQ ID NO. 6)</u>
FN6	Biotin-SGSG-LQSK(-COOH) <u>(SEQ ID NO. 7)</u>
FN7	Biotin-SGSG-PEEK(-COOH) <u>(SEQ ID NO. 8)</u>
FN8	Biotin-SGSG-TGEK(-COOH) <u>(SEQ ID NO. 9)</u>
FN9	Biotin-SGSG-WDSR(-COOH) <u>(SEQ ID NO. 10)</u>
FN10	Biotin-SGSG-YLDK(-COOH) <u>(SEQ ID NO. 11)</u>
FN11	SGSG-ASAK(-COOH) <u>(SEQ ID NO. 12)</u>
FN12	SGSG-ASAR(-COOH) <u>(SEQ ID NO. 13)</u>
FN13	Biotin-SGSG-LYEIAR(-COOH) <u>(SEQ ID NO. 14)</u>
FN14	Biotin-SGSG-DFAEDK(-COOH) <u>(SEQ ID NO. 15)</u>
FN15	Biotin-SGSG-LTEFAK(-COOH) <u>(SEQ ID NO. 16)</u>
FN16	Biotin-SGSG-TEEQLK(-COOH) <u>(SEQ ID NO. 17)</u>
FN17	Biotin-SGSG-SSAYSR(-COOH) <u>(SEQ ID NO. 18)</u>

On page 35, please delete the paragraph beginning at line 4, and replace with:

The selection of specific binders from the n-CoDeR library was performed using streptavidin coated magnetic beads (Hawkins, R.E., Russel, S.J. and Winter, G. (1992) *J. Mol. Biol.*, **226**, 889-896). The construction and handling of the n-CoDeR scFv phage display library is described in Söderland *et al* (2000) *Nature Biotech.*, **18**, 852-856. Three consecutive rounds of selection were performed; Selection 1. The n-CoDeR™ phage library (Lib 2000) was first pre-selected against an irrelevant biotinylated peptide (biotin-GIVKYLYEDEG (SEQ ID NO. 19), 10^{-7} M). The peptide was captured on streptavidin magnetic beads and the beads were removed by centrifugation. This pre-selection removes binders against streptavidin, biotin and the SGSG linker.